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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.40155 Seconds

(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-2

Perfect score: 578
Sequence: 1 QDWLTFQKKHKLNTBVDN.....TCVCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	96.2	104	1	RN30_RANPI
2	292	50.5	111	1	RNP0_RANCA
3	285.5	49.4	111	1	LECS_RANCA
4	269.5	46.6	111	1	RNPL_RANCA
5	149	25.8	119	1	RNP_IGUG
6	131	22.7	124	1	RNP_IGALU
7	130.5	22.6	145	1	ANGR_MOUSE
8	130.5	22.6	146	1	ANGI_CERAE
9	128	22.1	148	1	ANGI_BOVIN
10	126	21.8	128	1	RNP_MYOCO
11	125	21.6	124	1	RNP_BALAC
12	121.5	21.0	146	1	ANGI_MACMU
13	120	20.8	128	1	RNP_PROGU
14	119.5	20.7	145	1	ANGI_MOUSE
15	119	20.6	128	1	RNP_CAVPO
16	118.5	20.5	146	1	ANGI_PAPHA
17	117	20.2	124	1	RNP_CHIBR
18	116	20.1	125	1	ANGI_RABIT
19	116	20.1	128	1	RNP_HYDHY
20	114	19.7	124	1	RNP_HIPAM
21	114	19.7	146	1	ANGI_MOTFA
22	113	19.6	147	1	ANGI_HUMAN
23	113	19.6	147	1	ANGI_PANTR
24	112	19.4	124	1	RNP_PIG
25	112	19.4	150	1	RNP_BOVIN
26	112	19.4	156	1	RNP_MYOG
27	111.5	19.3	147	1	RNL4_HUMAN
28	111	19.2	128	1	RNP_HORSE
29	111	19.2	128	1	RNP_HYSCR
30	111	19.2	156	1	ECP3_MOUSE
31	111	19.2	167	1	RNBR_BOVIN
32	110.5	19.1	123	1	ANGI_PIG
33	110.5	19.1	155	1	ECPI_MOUSE

34	110	19.0	141	1	RNBR_GIRCA	Q29542 giraffa cam
35	110	19.0	146	1	ANGI_SAGOE	O8W62 saguinus oe
36	110	19.0	151	1	RNBR_AXIPR	P87350 axis porcin
37	109	18.9	123	1	ANGI_BOVIN	P80929 bos taurus
38	109	18.9	124	1	RNPA_CAVPO	P00678 cavia porce
39	109	18.9	124	1	RNP_AEPME	P07847 aepyceros m
40	109	18.9	124	1	RNP_ANTAM	P00668 antilocapra
41	109	18.9	124	1	RNP_SHEEP	P00661 ovis aries
42	109	18.9	146	1	ANGI_SAIISC	O8W60 salmtr sci
43	108.5	18.8	150	1	RNKG_SAIISC	O46529 salmtr sci
44	108	18.7	124	1	RNP_BUBBU	P00657 bubalus bub
45	108	18.7	124	1	RNP_CONTA	P00660 connochaete

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	104 AA
RN30_RANPI					
AC	P22069				
DT	01-ANG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1995 (Rel. 31, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RX	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelet W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases."				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; PubMed=1438177;				
RA	Mosimann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.;				
RT	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos."				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Mosimann S.C., Ardelet W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity."				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; RnaaseA.				
DR	Pfam: PF00074; RnaaseA: 1.				
DR	Prodom: PD000535; RnaaseA: 1.				
DR	SMART: SM00092; Rnaase_Pc: 1.				
DR	PROSITE: PS00127; Rnaase_PANCREATIC: 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3d-structure.				
FT	MOD_RSS				
FT	ACT_SITE				
FT	ACT_SITE				
FT	ACT_SITE				
FT	ACT_SITE				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				

FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2P9E566B4 CRC64;

Query Match 96.2%; Score 556; DB 1; Length 104;
 Best Local Similarity 96.2%; Pred. No. 1e-52;
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHHITRDVDCNNIMSTNLFHCKDKNTFYSPPEPYKAICGIIASKNVLT 60
 D 1 QDWLTFQKHHITRDVDCNNIMSTNLFHCKDKNTFYSPPEPYKAICGIIASKNVLT 60
 QY 61 SEFLSDCANTSRCKKTKLKSTNTFCVTCENAPVHFVGVC 104
 D 61 SEFLSDCANTSRCKKTKLKSTNTFCVTCENAPVHFVGVC 104

RESULT 2
 RNPO_RANCA STANDARD; PRT: 111 AA.

AC P11916; 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding lectin) (SBL-C).
 OS Rana catesbeiana (bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Egg;
 RX MEDLINE=87299649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., Takayanagi G., Hakomori S.;
 RT "Amino acid sequence of stallic acid binding lectin from frog (Rana catesbeiana) eggs";
 RL Biochemistry 26:2189-2194(1987).
 RN [2]
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-quanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN [3]
 RP CHARACTERIZATION.
 RC TISSUE-Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of stallic acid-binding lectin from Rana catesbeiana eggs";
 RL Glycobiology 3:37-45(1993).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=88437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
 RL J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR: A27121; A27121.
 DR PDB: 1BC4; 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.
 FT MOD_RES 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729CEP4 CRC64;

Query Match 50.5%; Score 292; DB 1; Length 111;
 Best Local Similarity 49.5%; Pred. No. 1.6e-24;
 Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKHHITRDVDCNNIMSTNLFHCKDKNTFYSPPEPYKAICGIIASKNV 56
 D 1 QDWLTFQKHHITRDVDCNNIMSTNLFHCKDKNTFYSPPEPYKAICGIIASKNV 59
 QY 57 VLTSEFLSDC---NTSRCKKTKLKSTNTFCVTCENAPVHFVGVC 104
 D 60 VLTSEFLSDC---NTSRCKKTKLKSTNTFCVTCENAPVHFVGVC 110

RESULT 3

LECS_RANJA STANDARD; PRT: 111 AA.

AC P18839; 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stallic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese redfish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE-Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H., Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.

DR HSSP; P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Sialic acid; Lectin.
 FT MOD_RES 1
 FT ACT_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 35 35 BY SIMILARITY.
 FT ACT_SITE 103 103 BY SIMILARITY.
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.4%; Score 285.5; DB 1; Length 111;
 Best Local Similarity 45.0%; Pred. No. 8.1e-24;
 Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

OY 1 ODMLTFFQKKHLTNRDVCNNIMSTNLF---HCKDKNTFLYSRPEPVKAICGIIASKN 56
 Db 1 QNMAKFEKHHPTNSINCNITIMDKSIYVGGCKERTFTLISATTYKALCSGASTNRN 60

OY 57 VLTSEFYLSDC---NVTSRPCKYKLLKSTNTPCVTCENQAPVHFVGVGHC 104
 Db 61 VLSTTRQLMNCIRSATAPRCPYNSRTETNVICVKCENRLPVPFAGIGRC 111

RESULT 4
 RNP_L_RANCA STANDARD; PRT; 111 AA.
 AC P16626;
 DT 01-APR-1990 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nita R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RA Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (*Rana catesbeiana*)
 RT liver.";
 RL J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0085; JX0085.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 FT HydroLase: Nuclease; Endonuclease.
 FT MOD_RES 1
 FT ACT_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 35 35 BY SIMILARITY.
 FT ACT_SITE 104 104 BY SIMILARITY.
 FT DISULFID 19 72 BY SIMILARITY.
 FT DISULFID 34 82 BY SIMILARITY.
 FT DISULFID 52 97 BY SIMILARITY.
 FT DISULFID 94 111 PROBABLE.
 SQ SEQUENCE 111 AA; 12461 MW; D64BA2456C10788 CRC64;

Query Match 46.6%; Score 269.5; DB 1; Length 111;
 Best Local Similarity 43.2%; Pred. No. 4.1e-22;
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

OY 1 ODMLTFFQKKHLTNRDVCNNIMSTNLF---HCKDKNTFLYSRPEPVKAICGIIASKN 56
 Db 1 QNMAKFEKHHPTNSINCNITIMDKSIYVGGCKERTFTLISATTYKALCSGASTNRN 60

OY 57 VLTSEFYLSDC---NVTSRPCKYKLLKSTNTPCVTCENQAPVHFVGVGHC 104
 Db 61 ELSTTSFKLNTCLRDSITPRCPYHPSPDNNKICVKCEKOLPVPFVIGIGRC 111

RESULT 5
 RNP_IGUG STANDARD; PRT; 119 AA.
 AC P80287;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 OS Iguana iguana (Common Iguana).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=8517;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=94139745; PubMed=8307028;
 RA Zhao W., Beintema J.J., Hofsteenge J.;
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic
 RT ribonuclease.";
 RL Eur. J. Biochem. 219:641-646(1994).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP: P00656; 1LSQ.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease.
 FT MOD_RES 1
 FT DISULFID 25 80 PYROLIDONE CARBOXYLIC ACID.
 FT DISULFID 39 91 BY SIMILARITY.
 FT DISULFID 57 106 BY SIMILARITY.
 FT ACT_SITE 10 10 BY SIMILARITY.
 FT ACT_SITE 40 40 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 SQ SEQUENCE 119 AA; 13324 MW; 6072F5B7B15BD5A CRC64;

Query Match 25.8%; Score 149; DB 1; Length 119;
 Best Local Similarity 30.7%; Pred. No. 3.2e-09;
 Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

OY 1 ODMLTFFQKKHL-----TNRDVCNNIM---STNLFCKDKNTFLYSRPEPVKAIC--K 49
 Db 1 QDMSSFOKKHLDYETTSNMAVCDLMOGRNLNPTPKCKRNTFVHASPSEIQVCGSG 60

OY 50 GIASKNVLTSE--FYLSDC---NVTSRPCKYKLLKSTNTPCVTCENQAPVHF 98
 Db 61 GTHVEDNLVDSNESFDLTDCKNVGTAAPSCKYNGTGTCKRTRIRACEENNQPVHF 114

RESULT 6
 RNP_GALMU STANDARD; PRT; 124 AA.
 ID RNP_GALMU

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AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Galesa musteloides (Culis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Galesa.
OX NCBI_Taxid=10146;
RN [1]
RP SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and cuis ribonuclease.";
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00827; NR01.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA: 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc: 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR KAT: K00001; RNaseA: 1.
FT Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT ACT_SITE 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.7%; Score 131; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 2.8e-07;
Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

OY 4 LTRCKKH-----TNRDVCNNIM---STNLFHCKDKNTFYISREPPYKAICKGIIA 53
DB 6 MKFQRHMDSDGHDPTNTN--YCNEMYRRSMTOGRCPVNTFVHEPLEAVQAVC----S 59
OY 54 SKNV-----LTTSEFYLSDCNVTSR---CKYKLKSTNTFCVTGEN--QAPVH 97
DB 60 OKNVPCKNGQTCNYSMSMTITDCRYTSSSKYRNCSTKMTQAKSITVACEGIPSPVH 119
OY 98 F 98
DB 120 F 120

RESULT 7
ANGR_MOUSE STANDARD; PRT; 145 AA.
AC O64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: U22519; AAA91367.1;
DR HSSP: P03950; IAAV.
DR MGD: MGI:104984; Angrp.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA: 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc: 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolyase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT DISULFID 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 3.8e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

OY 30 CKDNKTFYISREPPYKAIC--KGIASKNV--LTTSEFYLSDCNVTSR---PCKYKLKKS 82
DB 63 CKDVNTFHDHTRKNKIKAIKCKGKSPYGRNLKISRSFOYTTCTYKGSPPRCRYRASKG 122
OY 83 TTFECVTCENQAPVHF 98
DB 123 FRYLIGCENGMPVHF 138

RESULT 8
ANGI_CERAE STANDARD; PRT; 146 AA.
AC O8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_Taxid=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";

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RL M01. Biol. Evol. 19:438-445(2002).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF441664; AAL61646.1;
KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KM Protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 1 24
FT MOD_RES 25 146
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;

Query Match 22.68; Score 130.5; DB 1; Length 146;
Best Local Similarity 30.78; Pred. No. 3.0e-07;
Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;

QY 5 TPEKHLTNTRDVDCNNIMSTNLFHCKDKMTFTYSPREPKAIC---KGIIASKNV-LTT 60
Db 53 TMRNRHLTSP-----CKDITFTIGHNRHKAICDGNAPYGENLRISK 97

QY 61 SEFYLSDCNVTs---RPCKYKLLKKSSTNFTVCENAPVH 97
Db 98 SPFOVTTCNLRGSGSPRPCCYRATRGSRNIVGCCENCLPVH 138

RESULT 9
ANGI_BOVIN STANDARD; PRT; 148 AA.
ID ANGI_BOVIN STANDARD; PRT; 148 AA.
AC P10152: O9GKP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin-1 precursor (Ec 3.1.27.-).
GN ANGI OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
OC Bovidae: Bovinae: Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver;
RA Chang S.-I.;
RT "Cloning, sequencing, and expression of bovine angiogenin.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-148.
RC TISSUE-Milk;
RX MEDLINE=89065101; PubMed=3197838;
RA Mes P., Danart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT "The complete amino acid sequence of bovine milk angiogenin.";
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RL FEBS Lett. 241:41-45(1988).
RN [3]
RN SEQUENCE OF 24-148.
RC TISSUE-Plasma;
RX MEDLINE=89375344; PubMed=2775757;
RA Bond M.D., Strydom D.J.;
RT "Amino acid sequence of bovine angiogenin.";
RL Biochemistry 28:6110-6113(1989).
RN [4]
RP CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC TISSUE-Plasma;
RX MEDLINE=89118214; PubMed=3064806;
RA Bond M.D., Vallee B.L.;
RT "Isolation of bovine angiogenin using a placental ribonuclease
RT inhibitor binding assay.";
RL Biochemistry 27:6282-6287(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=95224057; PubMed=7708754;
RA Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=96280645; PubMed=8688423;
RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT resonance spectroscopy.";
RL Biochemistry 35:8870-8880(1996).
RN [7]
RP -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
RP TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
RP ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
RP FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
RP MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
RP HYDROLYZING CELLULAR TRNAs. BINDS TIGHTLY TO PLACENTAL
RP RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: AF135124; AAC47631.1;
DR PIR: A32474; A32474.
DR PDB: 1AGT; 03-APR-96.
DR PDB: 1GIO; 07-DEC-96.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNaseA_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 1 24
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;

Query Match 22.18; Score 128; DB 1; Length 148;
Best Local Similarity 34.08; Pred. No. 7.1e-07;
```

Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

QY 16 DVOCNNIMSTNLF--HCKDKNTFIYSRPEPKAICKGIASKN-----VLTSEYVL 65
 DB 47 DEYFNMKNRRLTRPKDRNTFTHGKNDKACE-----DRNGQPYRGDIRISKSEFOI 102
 QY 66 SDC---NVTSR-PCKYKLRKSTNFCVTCENQAPVHF 98
 DB 103 TICHHKGGSSRPFCRYGATEDSRIVYVGCENGLPVHF 139

RESULT 10

RNP_MYOCO STANDARD: PRT: 128 AA.
 ID RNP_MYOCO
 AC P00676:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASEL OR RN51.
 OS Musca domestica (Housefly) (Diptera).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Myocastoridae;
 OC Myocastor.
 OX NCBI_Taxid=10157;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=77065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT "Isolation, properties and primary structure of coypu and chinchilla
 pancreatic ribonuclease."
 RL Blochim. Biophys. Acta 453:400-409(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; IRSN.
 DR HSSP: P00656; IRSN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 34 34
 SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.8%; Score 126; DB 1; Length 128;

Best Local Similarity 29.9%; Pred. No. 9.9e-07;

Matches 33; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
 QY 6 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPKAICKGIASKN 57
 DB 8 FENOHHMSRSPSPINPVCNEMKSRMKGCRKCPVTFVHEPLADYQAVC----FOKNV 63
 QY 58 L-----TSEFYLSDCNVTSRP---CKYKLRKSTNFCVTCENQ--APVHF 98
 DB 64 LCKNGQNTCYOSNSNMHITDCHRVTSNSGDPNCSYRTSQEKSIVVACGNPYVPHF 120

RESULT 11

RNP_BALAC

ID RNP_BALAC STANDARD: PRT: 124 AA.

AC P00673:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASEL OR RN51.
 OS Musca domestica (Housefly) (Diptera).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balanopteridae; Balanoptera.
 OX NCBI_Taxid=9767;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=7627855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lessor-rorqual) pancreatic
 ribonuclease."
 RL Biochem. J. 157:317-323(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00818; NRMHK.
 DR HSSP: P00656; IRSN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 76 76
 SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 21.6%; Score 125; DB 1; Length 124;

Best Local Similarity 28.6%; Pred. No. 1.2e-06;

Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;
 QY 4 LTFOKHLTNTRDVD-----CNNIMSTNLF--HCKDKNTFIYSRPEPKAICKGIASK 55
 DB 6 MKFDROHMDSONSGNPNPNCNOMMKRKTQGRKCPVNTFVHESLEDYQAVC-----SQK 61
 QY 56 NVL-----TSEFYLSDCNVTSRP---CKYKLRKSTNFCVTCENQ--APVHF 98
 DB 62 NVLCKNGRTNCEBSNSTMHITDCHROTSSKYVPCAYTSQKEKHIIIVACGNPYVPHF 120

RESULT 12

ANGI_MACMU STANDARD: PRT: 146 AA.

AC O8WN63;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG OR RNASE5.
 OS Musca musca (Housefly) (Diptera).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_Taxid=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-21918422; PubMed-11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RL primate evolution."; Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 CC -----
 DR EMBL: AF441667; AAL61649.1;
 KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 KM Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 146
 FT MOD_RES 25 25
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 138 138
 FT DISULFID 50 105
 FT DISULFID 63 116
 FT DISULFID 81 131
 SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;
 Query Match 21.0%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 3.5e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;
 QY 5 TFGKHLNTRDYDCNNIMSTNLFHCKDKNTFTYSRPEPKAIC--KGIASKNV-LTT 60
 DB 53 TMRRLHUTSP-----CKDINTFVHGNNHHTALICGDSGPGYGNLRIST 97
 QY 61 SEFYLSDCNVT---RPCKYKLLKSTNTFCVTCEADAPVH 97
 DB 98 SPFOVTTCKLRGSGPRPCQYRATRGSRNITVGCENGLPVH 138
 RESULT 13
 RNP_PROGU STANDARD; PRT; 128 AA.
 AC P04059;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASE1 OR RN51.
 OS Proechimys gualatae (Cassiragua).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.
 OX NCBI_TaxID=10163;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=83000399; PubMed=7115727;
 RA Beintema J.J., Knol G., Martena B.;
 RT "The primary structures of pancreatic ribonucleases from African
 RT porcupine and castiragua, two hystriocorniph rodent species."; Biochim. Biophys. Acta 705:102-110(1982).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00821; NRKS.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam: PF00794; RnaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RnaseA; 1.
 DR SMART: SM00092; Rnase_Pc; 1.
 DR PROSITE: PS00127; Rnase_PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 34 34
 SQ SEQUENCE 128 AA; 14244 MW; 2DB58093A9D3C936 CRC64;
 Query Match 20.8%; Score 120; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 4.3e-06;
 Matches 35; Conservative 16; Mismatches 36; Indels 28; Gaps 7;
 QY 6 FOKKHL-----TNRDYDCNNIM-STNLF--HCKDKNTFTYSRPEPKAICKGIASKNV 57
 DB 8 FOKHDISSGSPSTNPVCNAMKSRNMTGERCKPVNTFVHEPLADQAVC---FQKNV 63
 QY 58 -----LTTSEFLSDCNVTSR---PCKYKLLKSTNTFCVTCEAD--APVHF 98
 DB 64 PCKNGSGCYESTSNMHTDCLRTLSNSKFPDCLYRTSOEKSIIIVACEGNPYVPH 120
 RESULT 14
 ANGI_MOUSE STANDARD; PRT; 145 AA.
 ID ANGI_MOUSE
 AC P21570;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-).
 GN ANG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA."; Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiogenins: discernment of functionally important residues and
 RT regions."; Biochim. Biophys. Acta 1162:177-186(1993).
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U25316; AAA91366.1; -
DR PIR: A35932; A35932.
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR HydroLase: Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16228 MW; 069442608B764938 CRC64;

Query Match 20.7%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 5.6e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

QY 9 KHLNTRDQVD-----CNINMSTNLF--HCKDKMTFTYSRPEPKAIC--KGIASKN 56
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 32 KFLQHHADARKGDDRCERMKRSLTSPCKDVNTFTIHGNKSNKAIKICANGSPYREN 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 57 V-LTSEFYLSDCNVTST---RPCKYKLRKSTNFTCVTCENQAPVHF 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 92 LRMSKSPFYQVYTKHTGCGSPRPQCYRASAGFRHVIVACENGCLPVHF 138

RESULT 15
RNPB_CAVPO STANDARD; PRT; 128 AA.
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77185023; PubMed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gastra W.,
RA Beintema J.;
RT Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation.;
RL Eur. J. Biochem. 75:91-100(1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
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CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
DR HSSP: P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW HydroLase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT ACT_SITE 21 21
FT CARBOHYD 34 34
FT VARIANT 64 64
SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;

Query Match 20.6%; Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 5.5e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;

QY 4 LTFPKHL-----TNRDQDNNIM---STNLFHCKDKMTFTYSRPEPKAICKGIAS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 MKFORQHMDEPGSPSSNSN-CNVMMIRNMTOGRCKPVNTEFVESLADVOAVC---FQ 60
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 55 KNVV-----TSEEFYLSDCNVTST---CKYKLRKSTNFTCVTCENQ--APVHF 98
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 KNVCKKNGQNCYGSYRMRITDCRVYSSSKFRPCSTRMSQAQKSIIVACEGDPYVVF 120

Search completed: June 25, 2003, 14:50:02
Job time : 17.4016 secs
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